

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 3, 2000, 06:22:02 : Search time 10069.4 Seconds
(without alignments)
3254.293 Million cell updates/sec

Title: US-09-227-881-1
Perfect score: 5300
Sequence: 1 atcttgctcagttacctc.....cagcaccctctcagcacagc 5300

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7189864 segs, 3091403243 residues
Total number of hits satisfying chosen parameters: 14379728

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST: *
1: gb_est1: *
2: gb_est2: *
3: gb_est3: *
4: gb_est4: *
5: gb_est5: *
6: gb_est6: *
7: gb_est7: *
8: gb_est8: *
9: gb_est9: *
10: gb_est10: *
11: gb_est11: *
12: gb_est12: *
13: gb_est13: *
14: gb_est14: *
15: gb_est15: *
16: gb_est16: *
17: gb_est17: *
18: gb_est18: *
19: gb_est19: *
20: gb_est20: *
21: gb_est21: *
22: gb_est22: *
23: gb_est23: *
24: gb_est24: *
25: gb_est25: *
26: gb_est26: *
27: gb_est27: *
28: gb_est28: *
29: gb_est29: *
30: gb_est30: *
31: gb_est31: *
32: gb_est32: *
33: gb_est33: *
34: gb_est34: *
35: gb_est35: *
36: gb_est36: *
37: gb_est37: *
38: gb_est38: *
39: gb_est39: *
40: gb_est40: *
41: em_est4a: *
42: em_estfun: *
43: em_esthum1: *

44: em_esthum2: *
45: em_esthum3: *
46: em_esthum4: *
47: em_esthum5: *
48: em_esthum6: *
49: em_esthum7: *
50: em_esthum8: *
51: em_esthum9: *
52: em_esthum10: *
53: em_esthum11: *
54: em_esthum12: *
55: em_esthum13: *
56: em_esthum14: *
57: em_esthum15: *
58: em_esthum16: *
59: em_esthum17: *
60: em_esthum18: *
61: em_esthum19: *
62: em_esthum20: *
63: em_estin1: *
64: em_estin2: *
65: em_estin3: *
66: em_estin4: *
67: em_estom: *
68: em_estov1: *
69: em_estov2: *
70: em_estp1: *
71: em_estp12: *
72: em_estp13: *
73: em_estp14: *
74: em_estp15: *
75: em_estro1: *
76: em_estro2: *
77: em_estro3: *
78: em_estro4: *
79: em_estro5: *
80: em_estro6: *
81: em_estro7: *
82: em_estro8: *
83: em_estro9: *
84: em_estro10: *
85: em_estro11: *
86: em_estro12: *
87: em_estro13: *
88: gb_gss1: *
89: gb_gss2: *
90: gb_gss3: *
91: gb_gss4: *
92: em_gss1: *
93: em_gss2: *
94: em_gss3: *
95: em_gss4: *
96: gb_gss5: *
97: gb_gss6: *
98: gb_gss7: *
99: gb_gss8: *
100: gb_gss9: *
101: gb_gss10: *
102: gb_gss11: *
103: gb_gss12: *
104: gb_gss13: *
105: gb_gss14: *
106: gb_gss15: *
107: gb_gss16: *
108: gb_gss17: *
109: gb_gss18: *
110: gb_gss19: *
111: gb_gss20: *
112: gb_gss21: *
113: gb_gss22: *
114: gb_gss23: *
115: gb_gss24: *
116: em_gss5: *

117: em_gss6:*
118: em_gss7:*
119: em_gss8:*
120: em_gss9:*
121: em_gss10:*
122: em_gss11:*
123: em_gss12:*
124: em_gss13:*
125: em_gss14:*
126: em_gss15:*
127: em_gss16:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	180.8	3.4	660	88	A0057239 CIT-HSP-2
2	179.8	3.4	539	96	A0379787 RPT11-15
3	179	3.4	645	100	A0636457 RPT11-15
4	179	3.4	678	96	A0387027 RPT11-15
5	178.4	3.4	537	25	AW978041 EST390150
6	177.6	3.4	516	89	A0112451 CIT-HSP-2
7	177.4	3.3	577	91	A0265389 CITBI-E1
8	177.2	3.3	548	11	A1583291 tC56902.x
9	176.6	3.3	434	90	A0199435 RPT11-58
10	176.6	3.3	591	25	AW979191 EST391301
11	176	3.3	521	21	AW273360 x138A04.x
12	176	3.3	551	39	T53829 yB55610.s1
13	175.8	3.3	589	91	A0283440 RPT11-79
14	175.4	3.3	386	98	A0474222 CITBI-E1
15	175.2	3.3	711	97	AQ15030 RPT11-2
16	175	3.3	388	19	AW069227 C141h09.x
17	175	3.3	421	23	AW674631 b41a11.x
18	175	3.3	447	24	AW820784 RC2-ST030
19	175	3.3	454	12	A1634187 t555A08.x
20	175	3.3	474	10	A1573713 t173A05.x
21	175	3.3	527	11	A1523813 t996d09.x
22	174.8	3.3	432	9	A1300818 g47C06.x
23	174.8	3.3	435	9	A1300992 g095A06.x
24	174.6	3.3	424	10	A1431513 t455F04.x
25	174.6	3.3	677	110	B66612 CIT-HSP-201
26	174.2	3.3	342	6	AA846923 ge06d01.s
27	173.8	3.3	460	110	B15692 345N8-TP CI
28	173.8	3.3	565	25	AW953220 EST365290
29	173.6	3.3	368	21	AW270385 xp74f06.x
30	173.6	3.3	374	37	F35684 HSPD32531 H
31	173.4	3.3	384	7	AA862029 c146604.s
32	173.4	3.3	427	5	AA550989 nj35d12.s
33	173.4	3.3	436	88	A0021084 CIT-HSP-2
34	173.4	3.3	486	8	A1049955 an38e01.x
35	173.4	3.3	642	110	B59854 CIT-HSP-345
36	173.4	3.3	836	102	A0781745 HS-3122.A
37	173.2	3.3	410	102	A1355246 q474b06.x
38	173.2	3.3	430	13	A1859906 wM23C01.x
39	173.2	3.3	508	100	A0632598 RPT11-4
40	173.2	3.3	784	101	A0738890 HS-5382.B
41	172.8	3.3	496	4	AA486819 ab19c10.x
42	172.8	3.3	624	96	A0373399 RPT11-15
43	172.6	3.3	300	7	AA937809 nw89b02.s
44	172.4	3.3	397	10	A1417469 tH33h09.x
45	172.4	3.3	439	14	A1961983 wt41a12.x

ALIGNMENTS

RESULT 1
A0057239

LOCUS A0057239 660 bp DNA
DEFINITION CIT-HSP-2340D14.TF CIT-HSP Homo sapiens genomic clone 2340D14, DNA
SEQUENCE
ACCESSION A0057239
VERSION A0057239.1 GI:3353765
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 660)
Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K.,
Golden,K., Berry,K., Granger,D., Sun,E., Wible,C., Shizuya,H.,
Simon,M. and Venter,J.C.
Use of a random BAC End Sequence Database for Sequence-Ready Map
Building (1998)
TITLE Unpublished (1998)
JOURNAL Other_GSSs: CIT-HSP-2340D14.TF
COMMENT Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13 Reverse
Class: BAC ends.

FEATURES
source 1..660
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2340D14"
/clone_id="CIT-HSP"
/sex="Male"
/cell_type="Sperm"
/note="Vector: pBelobAC11; Site_1: HindIII; Site_2:
HindIII"

BASE COUNT 116 a 188 c 150 g 206 t
ORIGIN

Query Match 3.4%; Score 180.8; DB 88; Length 660;
Best Local Similarity 86.0%; Pred. No. 8e-22;
Matches 215; Conservative 0; Mismatches 27; Indels 8; Gaps 1;

QY 1321 accgtgagctcactgcaacctctgctcccaagttcaagcaattctctctcagctctc 1380
|||||
DB 293 ATCTGACGTCACCTGCACTGCTGCTCCCGGTTCAACGATTCCTGTCACACCTCC 352
|||||

QY 1381 cgcgtgagctggtgactcagggcg-----cagcccggtcatttttgtattgtatla 1432
|||||
DB 333 CAAGTAGCTGGGATTACAGGCGCACACACACCGCCGCGTAATTTTGTATTTAAGTA 412
|||||

QY 1433 gggatggggtttccacattatggccgctggtcttgaaacctcagctcaggtatcca 1492
|||||
DB 413 GAGATGGGTTTACACCAATGTTGGCCAGGCTGCTCGAATCTCTACCTCAGATATCA 472
|||||

QY 1493 ccacactcagctccttaagtgtctggaattcaagcatgagttcacccgcccggccaagg 1552
|||||
DB 473 CCCACTGCTGCTCCCAAGTCTGGGATTTACAGGCTTGAGGCGCACTGGCCAGCCTAAT 532
|||||

QY 1553 gtcagtgctt 1562
|||||
DB 533 TTTTGTATT 542
|||||

RESULT 2
A0379787 539 bp DNA
LOCUS A0379787
DEFINITION RPT11-152C3.TF RPT11 Homo sapiens genomic clone RPT11-152C3,

Accession	DNA sequence.
Version	A0379787
Keywords	A0379787.1 GI:4350810
Source	GSS.
Organism	human.
Reference	Homo sapiens
Authors	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Title	1 (bases 1 to 539)
Journal	Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter, J.C.
Comment	Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building Unpublished (1997) Contact: Shaying Zhao, William Nierman, Mark Adams Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850 Tel: 301 838 0200 Fax: 301 838 0208 Email: hbe@tigr.org Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@jeng.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html Seq primer: SP6 Class: BAC ends.
Features	Location/Qualifiers
Source	1..539 /organism="Homo sapiens" /db_xref="GDB:7558034" /db_xref="taxon:9606" /clone="RPCI-11-152C3" /clone_id="RPCI-11" /sex="Male" /cell_type="Lymphocytes" /note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI; RPCI11 Human Male BAC Library"
Base Count	187 a 112 c 123 g 116 t 1 others
Origin	
Query Match	3.4%; Score 179.8; DB 96; Length 539;
Best Local Similarity	76.8%; Pred. No. 1.2e-21;
Matches	235; Conservative 0; Mismatches 63; Indels 8; Gaps
0Y	1280 agggtagaggtctgtgtcttaccctaccctgtatgtcttcaacccctgagctcaactgcaacc 1339
Db	327 AGAGCTCGCTCTGTGCACNCAGCTGGAGTTCACTGGCGGGATCTGGGCTCACAGCAAC 268
0Y	1340 tctgctcccaaggttcaagcaattctctgtcttaagctcccggtgtgcctgggaactcaag 1399
Db	267 TCTGCTCTCCCGGGTTCAAGCAATTCCTGCTCAGCTCCCGAGTGCCTGGGACCCAG 208
0Y	1400 gc-----gcagcccgagcttaattttgtatgttaagtagagatgggtttcacata 1451
Db	207 GCATGTGCCACATACCCGGCTAATTTTGTGATTTTAACTGTAAGAAACGGGTTTCACATG 148
0Y	1452 ttaagccgagctgtgtcttaacttccctgaactcaagttgaaccaccacactcagctcttaa 1511
Db	147 TTGGCAGAGCGTGTCTTAACCTCCTGACCTCAGGTGATCCACCAAGCCTTGCCCTCTAAA 88
0Y	1512 gtgcctggattaccaggaatgaatgacacgcccggcccaaggtcagtgtttaataagaa 1571
Db	87 GTGCGTGATTAACAGACTGAGTACACACCGCCGGCTCAATCCCTTTTTCAGTCTA 28
0Y	1572 taactt 1577
Db	27 TGAATT 22

[illegible]

KEYWORDS	GSS.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
	1 (bases 1 to 516)
	Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Ianher, K., Golden, K.,
	Berry, K., Granger, D., Suh, E., Wilde, C., Shizuya, H., Simon, M. and
	Venter, J.C.
TITLE	Use of a random human BAC End Sequence Database for Sequence-Ready
JOURNAL	Map Building
COMMENT	Unpublished (1998)
	Other GSSs: CIT-HSP-2372C9, TR
	Contact: Mark Adams
	Department of Eukaryotic Genomics
	The Institute for Genomic Research
	9712 Medical Center Dr., Rockville, MD 20850, USA
	Tel: 301 838 0200
	Fax: 301 838 0208
	Email: mdamads@tigr.org
	Clones are available from Research Genetics (Info@resgen.com). BAC
	End search page:
	http://www.tigr.org/tdb/hungen/bac_end_search/bac_end_search.html.
	See primer: M13-21
	Class: BAC ends.
FEATURES	Location/Qualifiers
source	1..516
	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/clone="2372C9"
	/clone_1lb="CIT-HSP"
	/sex="Male"
	/cell_type="Sperm"
	/note="Vector: pBelOBAC11; Site_1: HindIII; Site_2:
	HindIII"
BASE COUNT	87 a 145 c 118 g 166 t
ORIGIN	
Query Match	3.4%; Score 177.6; DB 89; Length 516;
Best Local Similarity	85.2%; Pred. No. 3e-21;
Matches 213: Conservative	0; Mismatches 29; Indels 8; Gaps 1.
Oy	1321 accctagctcactgtcaacctctgctcccaagttcaagaatctctcgtctcaagctcc 1380
Db	255 ATCTACAGCTCACTGCACACCTTGCTCCCGGTTCAAGGATTCCTGTCAAGCCTCC 314
Oy	1381 cgcgtagctcgggaactaagcg-----caagcccgctaatcttcttatgttaagta 1432
Db	315 CAAGTAGCTGGGATTAACAGCGCACACACACACGCCCGCTAATTTTATATTATTAGTA 374
Oy	1433 gagatggaggttcacacatattagcccgagtggttcttgaactctctgacctcagtgatca 1492
Db	375 GAGATGGGGTTTCACCATATTGGCCAGCGCTGCTGAACTCTGACCTTAGGTATCCA 434
Oy	1493 ccacctcagacctctcaagtgctggatattacaggaatgatacaccgcccgcgaag 1552
Db	435 CCCACCTTGCGCTCCCAAGGTGTGGATTAACAGCGCTGGGCACTGGCCCAAGCTTAA 494
Oy	1553 gtcaagtgttt 1562
Db	495 TTTTGCAATT 504
RESULT 7	
AQ265389/c	577 bp DNA GSS 27-OCT-1998
LOCUS	CITBI-21-2509010.TF CITBI-El Homo sapiens genomic clone 2509010,
DEFINITION	DNA sequence.
ACCESSION	AQ265389
VERSION	AQ265389.1 GI:3793589
KEYWORDS	GSS.
SOURCE	human.

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 577)	Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and Venter,J.C.	Use of a random human BAC End Sequence Database for Sequence-Ready Map Building	Unpublished (1998)	
	Other_GSSs: C17B1-E1-2509010.TR	Contact: Mark Adams	Department of Eukaryotic Genomics	
	The Institute for Genomic Sciences	9712 Medical Center Dr., Rockville, MD 20850, USA		
	Tel: 301 838 0200	Fax: 301 838 0208		
	Email: mdadams@tigr.org			
	Clones are available from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html . Seq primer: M13-21			
	Class: BAC ends.			
FEATURES	source	location/Qualifiers		
		1..577		
		/organism="Homo sapiens"		
		/db_xref="taxon:9606"		
		/clone="2509010"		
		/clone_11b="C17B1-E1"		
		/sex="male"		
		/cell_type="sperm"		
		/note="Vector: pBeloBAC11; Site_1: EcoRI; Site_2: EcoRI; Caltech Human BAC Library D"		
BASE COUNT	167 a	127 c	137 g	146 t
ORIGIN				
Query Match	3.3%	Score 177.4;	DB 91;	Length 577;
Best Local Similarity	75.1%;	Pred. No. 3.2e-21;		
Matches 238;	Conservative	0;	Mismatches 71;	Indels 8;
			Gaps 1;	
Qy	1321	acctaggtcactgtaaacactctgcctccaggttaagcaattctcgtctagccccc	1380	
Db	368	ATCTGGGCTCATGTGAACTCTGCCAGGTTCAATGATCTCTGCTCAGACCTTC	309	
Qy	1381	cgcgtagctgtggaactacagggc-----gcacgcccgcctaaatttctgatttgtagca	1432	
Db	308	CGAGTATCTAGAGACTACAGGCAACCCGCCACCAAGCCTGGCTAATTTTCTATTTAATA	249	
Qy	1433	ggagatggggttcacacataattagcccgagctggtcttgaactctcagacctcagtgatcca	1492	
Db	248	GAGACGGGGTTTCACCAATGTTGTGTGAGCGTGTGTTGAATCTGTGACCTCAGGCGATCCA	189	
Qy	1493	cccactcagcctctctaaagtctgtggttaagagcagatgcacggcccgccggcgaag	1552	
Db	188	CCCGCTTGGCTCCCAAGTCTGGGATTAAGGCATGAGCACTGACCCAGCCACGA	129	
Qy	1553	gtcagtggttaataagaaactctgtaatggttactaaaccaacagggaacagacaaa	1612	
Db	128	GATTAATTTTGTTAATTAATCTAGACTGGAGTCAAGTGCAGACAGCTCTCAGGCAAAAGGAGAAAT	69	
Qy	1613	agctgtgataaatttcag	1629	
Db	68	ACTAATTAAGTGTATGAG	52	
RESULT	8			
LOCUS	A1583291/C	548 bp	mRNA	EST
DEFINITION	tt56g02.x1 NC1 CGAP_HSC4 Homo sapiens cDNA clone IMAGE:2244818 3'			
	similar to RF:Q13538 Q13538 ORF2: FUNCTION UNKNOWN. ; contains Alu			
	repetitive element, mRNA sequence.			
ACCESSION	A1583291			

KEYWORDS	EST.	AT583291.1	GI:4569188
KEYWORDS	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1 (bases 1 to 548)		
	NCI-CCAP http://www.ncbi.nlm.nih.gov/nciccap .		
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),		
COMMENT	Tumor Gene Index		
	Unpublished (1997)		
	Contact: Robert Strausberg, Ph.D.		
	Tel: (301) 496-1550		
	Email: Robert.Strausberg@nih.gov		
	Tissue Procurement: Herbert Morse, M.D., Michael R. Emmert-Buck,		
	M.D., Ph.D.		
	cDNA Library Preparation: David B. Kitzman, Ph.D.		
	cDNA Library Arrayed by: Greg Lennon, Ph.D.		
	DNA Sequencing by: Washington University Genome Sequencing Center		
	Clone distribution: NCI-CCAP clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LLNL at:		
	www-bio.llnl.gov/bbrp/image/image.html		
	Insert Length: 664		
	Std Error: 0.00		
	Seq primer: -400P from Glbco		
	High quality sequence stop: 464		
	POLYA-No.		

FEATURES	SOURCE
Location/Qualifiers	
1..548	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone_image="224818"	
/clone_lib="NCI_CGAP_HSC4"	
/tissue_type="CD34+, CD38- from normal bone marrow donor"	
/lab_host="DH10B"	
/note="Organ: bone marrow; Vector: pAMP1; mRNA made from lymphoid tissue, cDNA made by oligo dT printing. directionally cloned. Size-selected on agarose gel, average insert size 500 bp. Primary library, non-amplified. cDNA library preparation: David B. Krizman, Ph.D. Reference: Krizman et al. (1996) Cancer Research 56:5380-5383."	
BASE COUNT	150 a 136 c 129 g 133 t
ORIGIN	

Query Match	3.3%	Score 177.2	DB 11	Length 548
Best Local Similarity	78.8%	Pred. No. 3.5e-21		
Matches 227	Conservative	0	Mismatches 53	Indels 8
				Gaps 1
QY 1277	gtgagggtaggggtgctgtgtcttaacaccactgtatgtctctacacactgagctcaatgca	1336		
DB 546	GAGGGAGTCTTATCTGTCTCAGGCTGAGTGCAGTGCATGATCTTGCTCACTGCA	487		
QY 1337	acctctgcctcccaaggttcaagaacattctctctgtctcagaacctccgcgtagcttgagacta	1396		
DB 486	ACCTCGCCTCAGAGGTTCAAGCAATTCCTCCGCCACACCTCTGAGCAGCTGAGACTA	427		
QY 1397	caggcg-----caggccgcgcgaattttgttatgttagtaagaatggaggtttacc	1448		
DB 426	CAGGGCCCCGCCACACACGCTGGCTTAATTTTGTATTTTAAATAGAGATGGGCTTTCCAC	367		
QY 1449	atatatgaccggctgtgtctctgaactctgaactctcaggtatgataccaccacctcagacctct	1508		
DB 366	ATGTTGGCCAGGCTGTGTGGAATCTCTGACTCAAGTGATCCACACCACTTGATCTCC	307		
QY 1509	aaagtgtcgtggaattacaggaatgagtcaaccgcgcgcgcgaaggtgtca	1556		
DB 306	AAAGTCTGTGGATTACAGCATATGAGCCACGTCGCCAGCCAGGATTTA	259		

RESULT	9				
AO199435/C					
LOCUS					
AO199435		434 bp	DNA	GSS	20-APR-1999

```

DEFINITION      RPC111-58F5.TJ RPC11-11 Homo sapiens genomic clone RPC11-58F5, DNA
sequence.
ACCESSION      AQ199435
VERSION        AQ199435.1
KEYWORDS       GSS.
SOURCE         human.
ORGANISM       Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 434)
                Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,
                Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C.
                Use of human BAC End Sequences for Sequence-Ready Map Building
                Unpublished (1998)
TITLE          Other_GSSs: RPC111-58F5.TK
JOURNAL
COMMENT
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are derived from the human BAC library RPC11-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Class: BAC ends.

```

FEATURES	source	location/Qualifiers
		1. 434
		/organism="Homo sapiens"
		/db_xref="GDB:7522012"
		/db_xref="taxon:9606"
		/clone="RPC1-11-58F5"
		/clone_11b="RPC1-11"
		/sex="Male"
		/cell_type="Lymphocytes"
		/note="Vector: pBACE3.6; Site_1: EcoRI; Site_2: EcoRI; RPCR11 Human Male BAC library"
BASE COUNT		118 a 108 c 114 g 94 t
ORIGIN		

	Query Match	3.3%	Score 176.6:	DB 90:	Length 434:
	Best Local Similarity	77.4%:	Pred. NO. 4.5e-21:		
	Matches 230:	Conservative	0:	Mismatches 35:	Indels 8:
				Gaps	1:
Oy	1292	tgtgtctacacctaaccttgcataccttcacacttgagctcaatcgacaacctctgctccag	1351		
Dd	427	tcttCACTCAGGCGTGGAGTCACATGGCACAGCATTTGGCTCTGTGCACAACCTGCTCCCTGG	368		
Oy	1352	gttcaagaacaattctcctgtctcaagcctcccgcgtagtgtggatacaggc-----gc	1403		
Dd	367	gTTCAAGAACAATTCTCOTGTCTCAGCCTCCCAAGTAGTGATTTACAGCACCGGCCAAC	308		
Oy	1404	accgccgcgaataatttttgtatgttaagtagagaaatgggggtttcacatataaecgcgcg	1463		
Dd	307	ATGCCCGGCTAATTTTGTATTTTGTAGTACAGATGGGGTTTACTATGTTGGCTGCGCTA	248		
Oy	1464	gtcttgaactccttgagocctaaagtagtatcaaccaccaactcaagccctccaagaatgtgtgatta	1523		
Dd	247	gTCTCGAACTCCGGACCTCAGGTGAATCCACGCTTGCCCTTCGMAAGTGTGGGATTA	188		
Oy	1524	caggcaatgatcatcagcgcgcgcgaagaagtgctaatlaaagaataacttgaa	1580		
Dd	187	CAGGTGTAGTAGTACCCTGCCCCAGCCAGAGAGTATGGGTTTTATCAGAGAAGATCTGA	131		

RESULT	10	
AW979191		
LOCUS	AW979191	
DEFINITION	EST191301	MAGE resequences, MAGP Homo sapiens CDNA, mRNA sequence.
	591 bp	mRNA
		EST
		02-JUN-2000

	ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
	REFERENCE	1 (bases 1 to 551)
	AUTHORS	Hillier,L., Lennon,G., Becker,M., Donaldson,M.F., Chapell,B., Chisgode,S., Dietrich,N., Dubucq,T., Favello,A., Gish,M., Hawkins, ' M., Hultman,M., Kucaba,T., Lacy,M., Le'M., Le'N., Merdis,E., Moore, ' B., Morris,M., Parsons,J., Prange,C., Rifkin,D., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thiersch-Weg,J., Trevisan,E., Underwood,R., Wohlmann,P., Waterston,R., Wilson,R. and Marra,M. Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996) 97044478
	TITLE	Contact: Wilson RK
	JOURNAL MEDLINE	Washington University School of Medicine 444 Forest Park Parkway, Box 850L, St. Louis, MO 63108 Tel.: 314 286 1800 Fax: 314 286 1810 Email: estewatson.wustl.edu
	COMMENT	Insert Size: 760 High quality sequence scraps: 380 Source: IMAGE Consortium, LINL This clone is available royalty-free through LINL ; contact the IMAGE Consortium (info@image.lnl.gov) for further information. Insert Length: 760 Std Error: 0.00 Seq primer: -2lmj3 High quality sequence stop: 380. Location/Qualifiers 1..551 /organism="Homo sapiens" /db_xref="GDB:497716" /db_xref="taxon:9606" /clone="IMAGE:77971" /clone_lib-"Stratagene liver (#937224)" /sex="male" /dev_stage="49 years old" /lab_host="SOLR cells (kanamycin resistant)" /note="Organ: Liver; Vector: pluscript SK; Site_1: ECORR /Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dT. Hepatectomy from normal male caucasian. Average insert size: 1.1 kb; Uni-ZAP XR vector: ~5' adaptor sequence: 5' GAATTCGGCAGCAG 3' -3' adaptor sequence: 5' CTCGAGTTTTTTT TTTT TTTT 3'
	BASE COUNT	119 a 134 c 127 g 163 t 8 others
	ORIGIN	
	Query Match	3.3%; Score 176; DB 39; Length 551;
	Best Local Similarity	80.7%; Pred. No. 5, 6e-21;
	Matches 221:	Conservative 0; Mismatches 45; Indels 8; Gaps 1;
Oy	1321 acctgagtcaactgtgaacctcgcctccaggttcaagaattcttcgtctcaagctccc	1380
Dd	47 atctcgcgctacactgcgaaccttgcctccagattcaaggatttcctcctcacgctcc	106
Oy	1381 cgcgtaagctggaaaccaagcg-----cagccccgctaatttgttatgttagta	1432
Dd	107 tgagTAGCCAGGATTACAGGTGCCGCCACCACACACACACTAATTTTGTATTATTAGA	166
Oy	1433 gagatgggggtttcacatatatgaccggcgctgtcttgaaacctccaaccagtgatcca	1492
Dd	167 gagATGGGGTTTCACTATGTTTGCCAAGGCTACTTGTACTCTCTGACCTCAGGTATCCA	226
Oy	1493 ccacaccacagcctctctaaagtctggaattacaagcatagtcacgcgcgccgccaagy	1552
Dd	227 CCCGCCTCAGCCTCCCAAAGTCTGGGATTAAAGCATATAGTCACCGCCCCTGGCCTTTC	286
Oy	1553 gtcaaigttaaagaataacttgaabgyttc 1586	
Dd	287 CTGACTTTTAACTGATCACCATTTTAAGTGGTAT 320	
RESULT	13	
	KO283440	

LOCUS	AO283440	589 bp	DNA	GSS	27-APR-1999
DEFINITION	RPc11.1-7965.TV	RPc11.1	Homo sapiens	genomic clone	RPc11-7965, DNA
ACCESSION	AO283440				
VERSION	AO283440.1	GI:3908257			
KEYWORDS	GSS.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
AUTHORS	Adams M.D., Rounsley S.D., Zhao S., Bass S., Linher K., Golden K., Berry K., Granger D., Suh E., Wille C., de Jong P. and Venter J.C.				
TITLE	Use of human BAC end Sequences for Sequence-Ready Map Building				
JOURNAL	Unpublished (1998)				
COMMENT	Other-GSS: RPc11-7965.TV Contact: Mark Adams Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0208 Email: mdamas@tigr.org Clones are derived from the human BAC library RPc11. For BAC library availability, please contact Pieter de Jong (pieter@edjlong.med.buffalo.edu). Clones may be purchased from BACpac Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tcdb/hungen/bac_end_search/bac_end_search.html Seq primer: SP6 Class: BAC ends.				
FEATURES	Location/Qualifiers				
source	1..589 /organism="Homo sapiens" /db_xref="GDB:7530100" /db_xref="taxon:9606" /clone="RPc11-7965" /clone_11b="RPc11-11" /sex="Male" /cell_type="Lymphocytes" /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; RPc11 Human Male BAC Library"				
BASE COUNT	146 a 126 c 136 g 181 t				
ORIGIN					
Query Match	3.3%; Score 175.8; DB 91; Length 589;				
Best Local Similarity	75.7%; Pred. No. 6e-21;				
Matches	234; Conservative 0; Mismatches 67; Indels 8; Gaps 1.				
QY	1280 agggatgagggtctgtgtcttacacctacctgtatgtcttacacctgagctcagcgaacc	1339			
DB	105 AGAGTCTTCTCTGTGGCCAGCGTGAGATACAGTGGTCGATGTACAGTCTACTCCAAAC	164			
QY	1340 tctgtctcccaaggttcaagcaattctctcgtgtctcagctcccggtagcttgaggactaag	1399			
DB	165 TCTGACTCCTCGGTTCAACAACATTCCTCGTTTGAGCCCCCGAGTACGTGGGATTACG	224			
QY	1400 ggc-----caagcccgcgtaattttgtatgtgtatgtagagaatggggtttcacata	1451			
DB	225 GTGCCTGCCACCATGCTAGCTAATTTTTTTGTATTTTACACAGATGGGGTTTCAACATA	284			
QY	1452 tttagccgagctgtcttgaacctccggaacctcaggtgatccacccacccctcagctctaa	1511			
DB	285 TTGGTCAGAGCTGTCTGGAACCTCGAAGCTCATGTGATGCACACCGTTCAGCTCCAAA	344			
QY	1512 gtgcctggagttacaggaatgagtcacgcgcgcgcgcgaagggtcagtggttaataagaa	1571			
DB	345 GTGCTGGGATTTACAGGCGGACGACCGTGCCTGGTCCAGGGGTGATGTTTATAGAA	404			
QY	1572 taacttgaa 1580				
DB	405 TAATCTGCA 413				

Mon Dec 4 08:51:36 2000

us-09-227-881-1.rst

Page 10

Db 65 CTTGCTGCTGTTTGGTA 48

Search completed: December 3, 2000, 10:14:55
Job time: 13973 sec